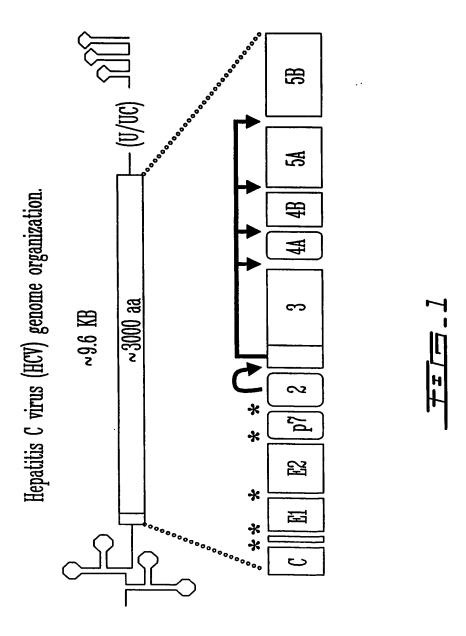
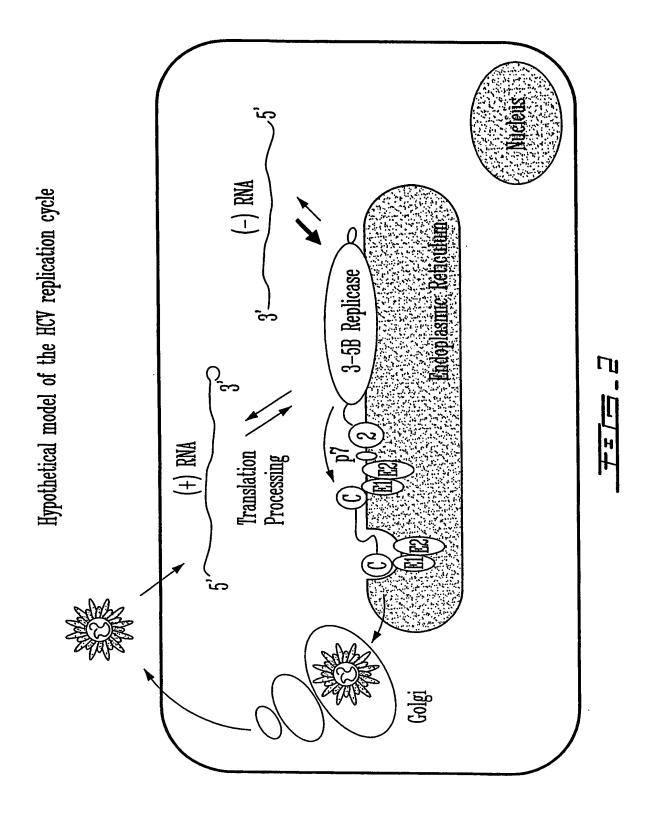
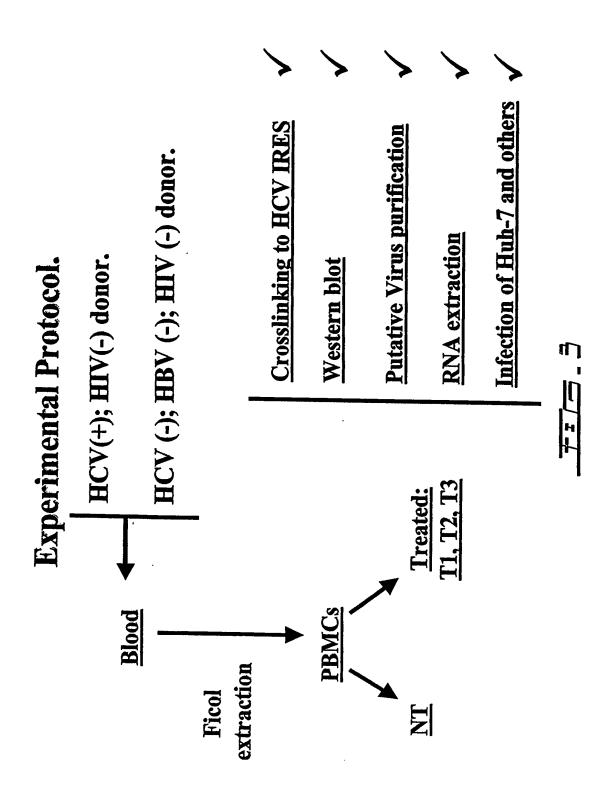
1 / 72



2/72

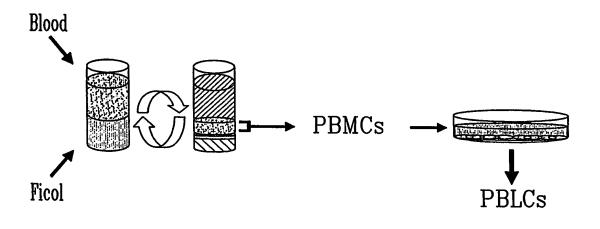


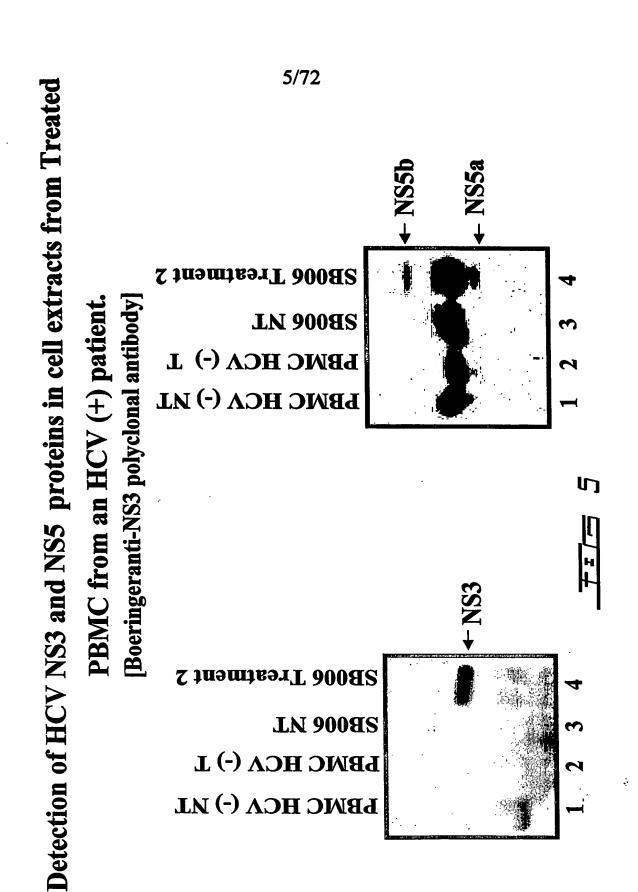
SUBSTITUTE SHEET (RULE 26)



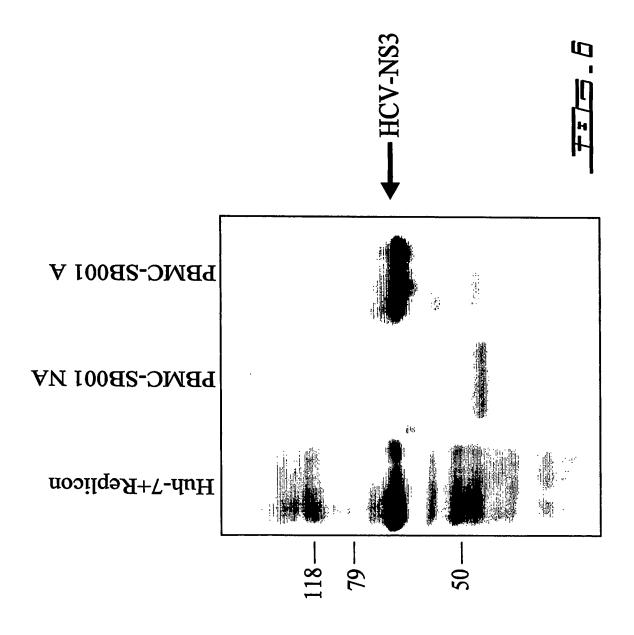
4/72

PBMC and PBLC purification from blood samples.



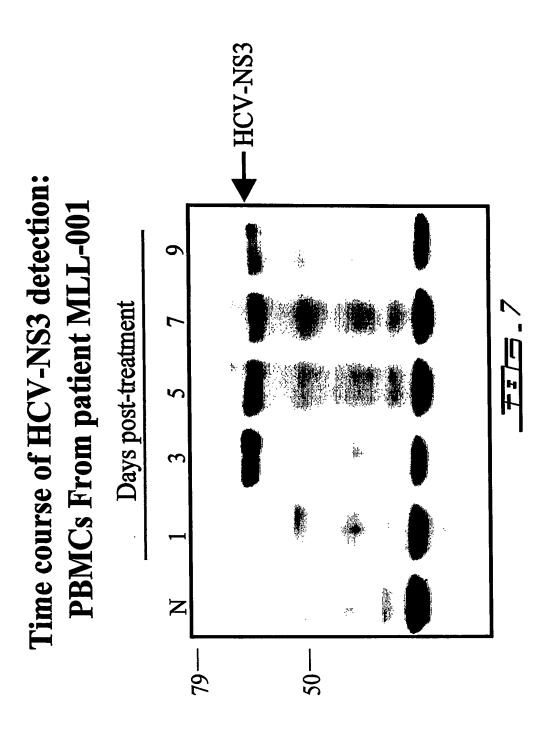


6/72

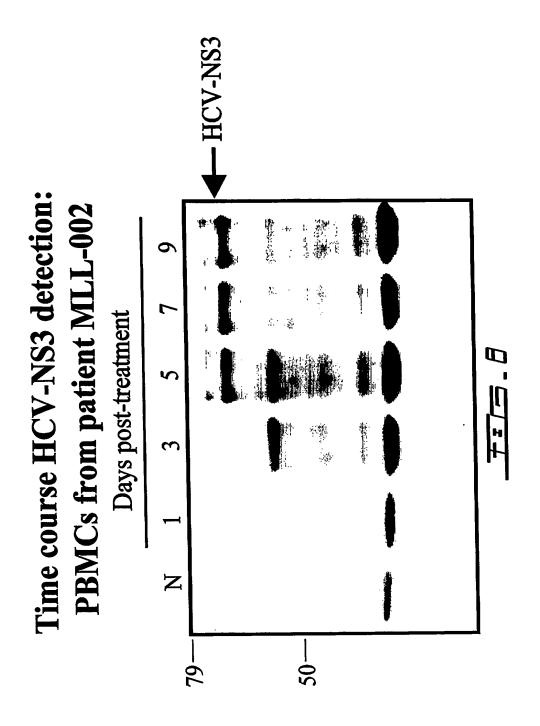


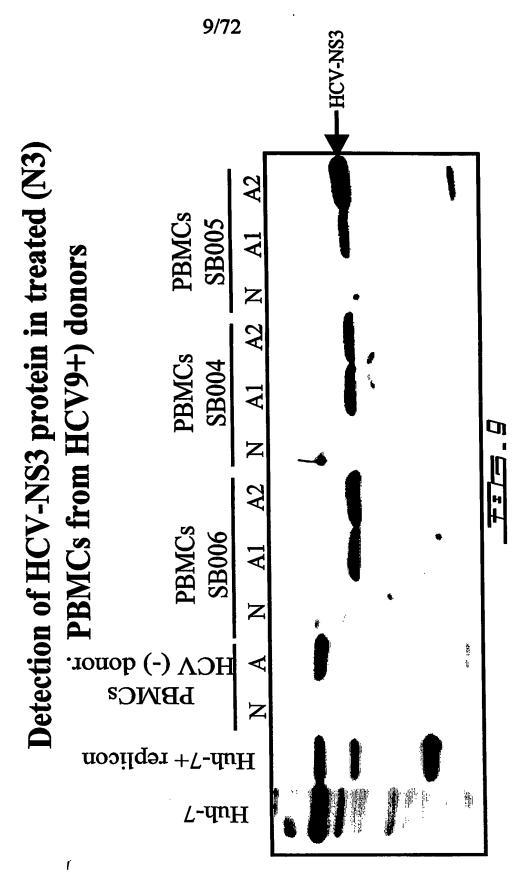
SUBSTITUTE SHEET (RULE 26)

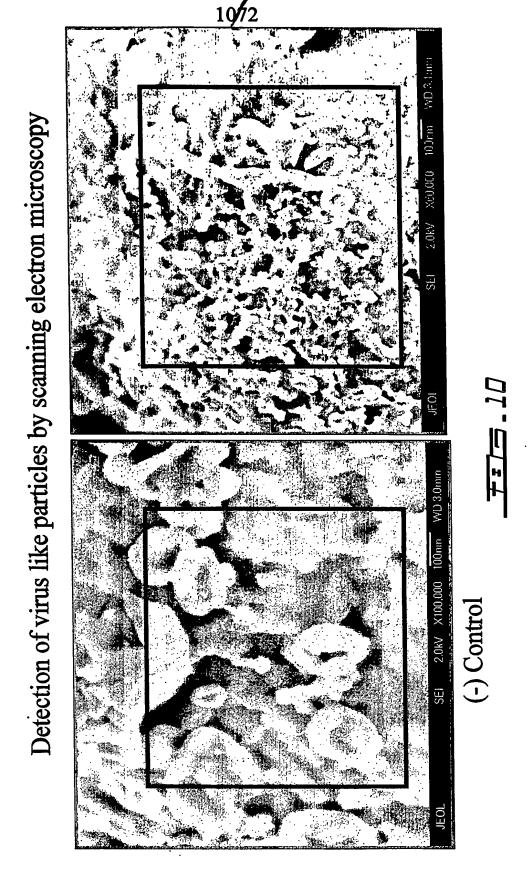




8/72

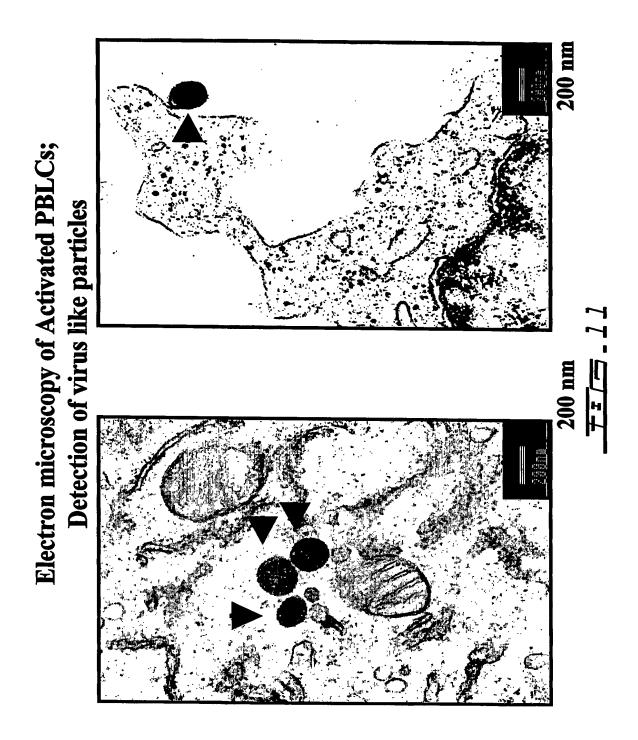




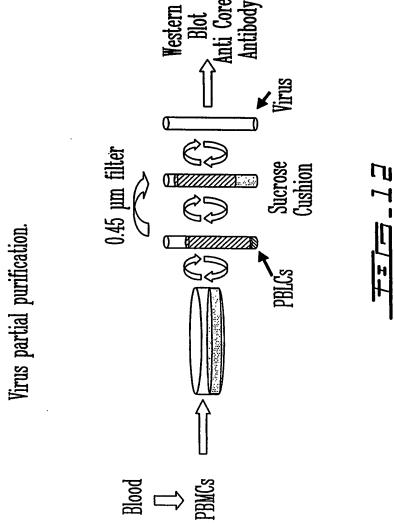


SUBSTITUTE SHEET (RULE 26)

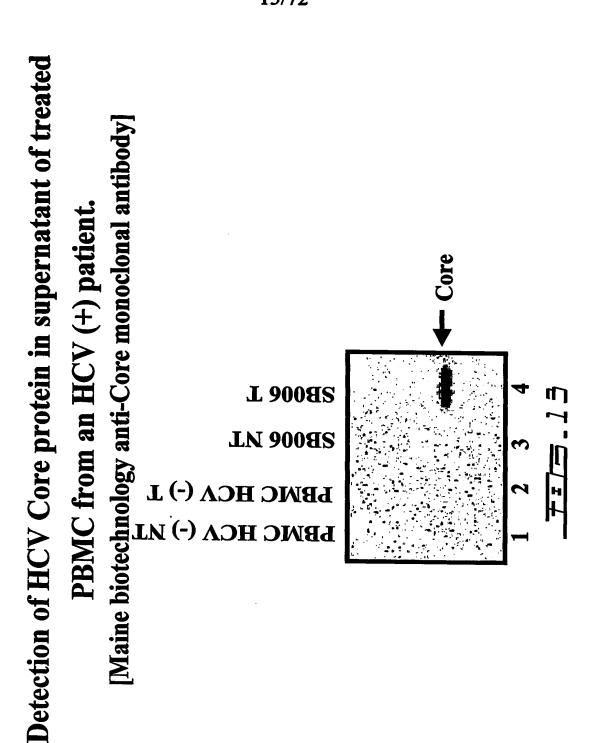
11/72



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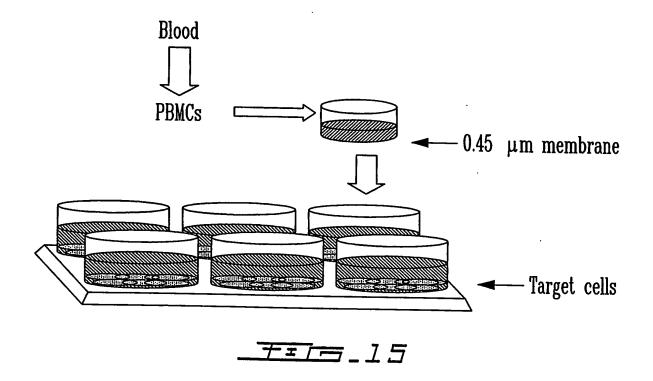


0.00

NA Quantification I (virus copies/ng total RNA)	Detection of	Core (wb) in supernatant	No	Yes	No	Yes	
tion I (virus c	HCV RNA	In PBMC	2x10 ³	2x10 ³	1.8 x10 ³	2x10 ²	
NA Quantifica	Patient	After 4 days	SB004 NT	SB004 T	SB006 NT	SB006 T	After 20 days

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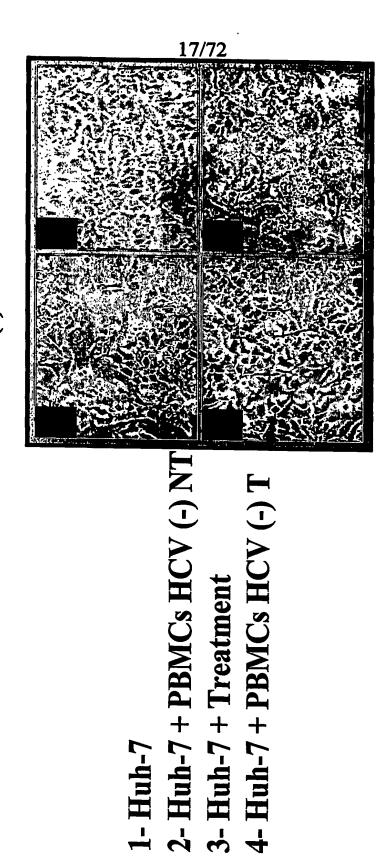
Infection assay; co-culture



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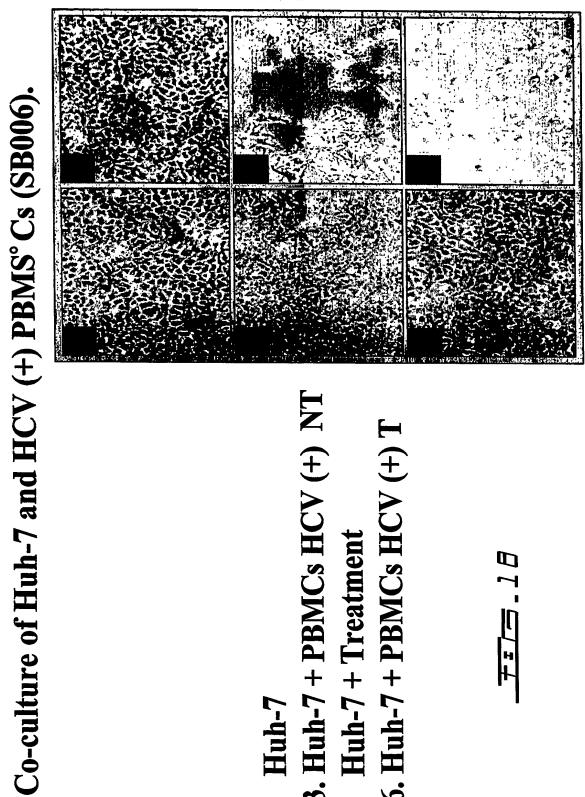
HCV RNA In MT-4 1600 0.00 RNA Quantification II (virus copies/ng total RNA) Detection of Core supernatant (wb) in Infection of MT-4 cells 2 N HCV RNA In PBMC 0.00 0.00 **SB001 NT** After 10 days After 20 days **SB001** T Patient **SB001 SB001**

Co-culture of Huh-7 and HCV (-) PBMCs.



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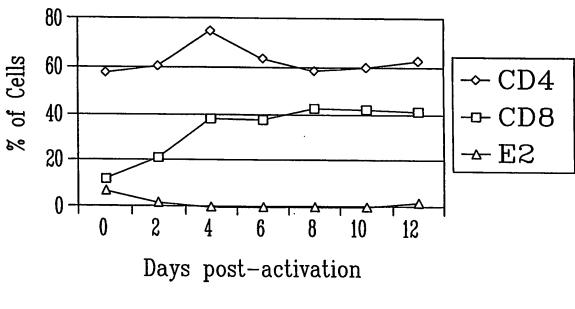
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2-3. Huh-7 + PBMCs HCV (+) NT
4. Huh-7 + Treatment
5-6. Huh-7 + PBMCs HCV (+) T

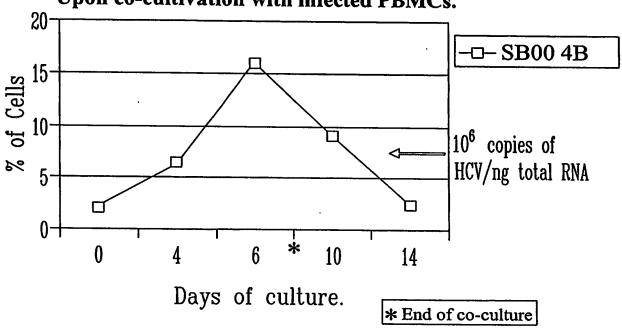
19/72

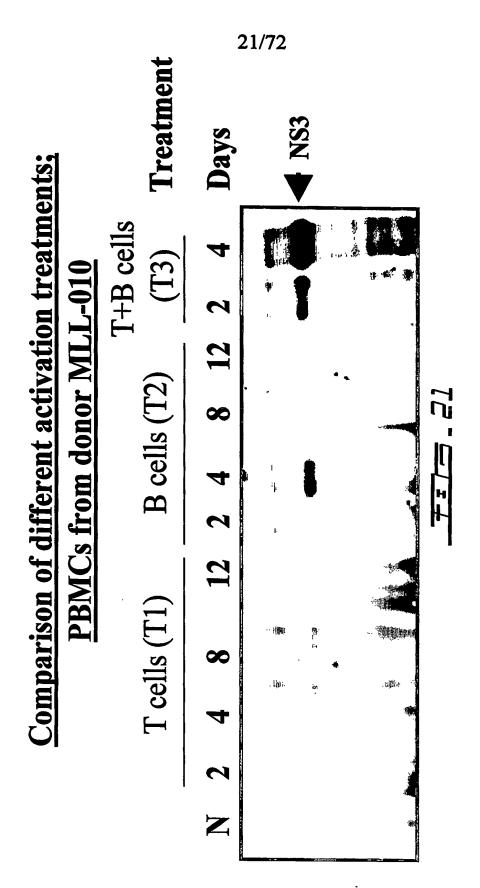
PHA Activation of PBMCs from patient SB004; HCV is not in T cells



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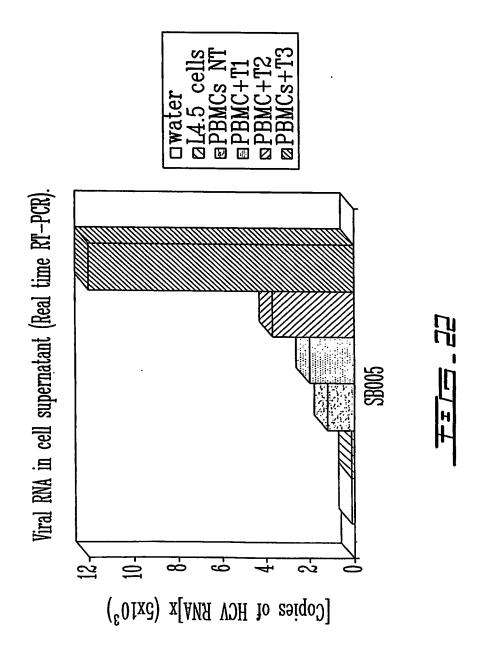
Detection of HCV (E2) on Daudi cells Upon co-cultivation with infected PBMCs.



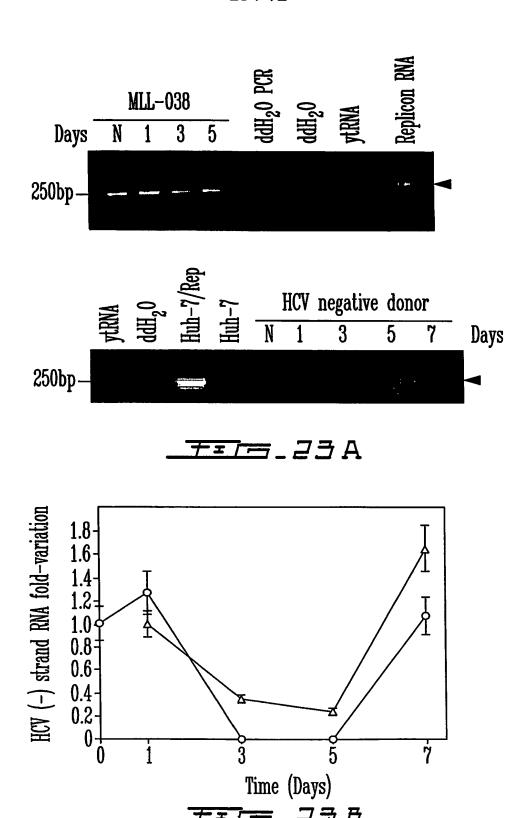


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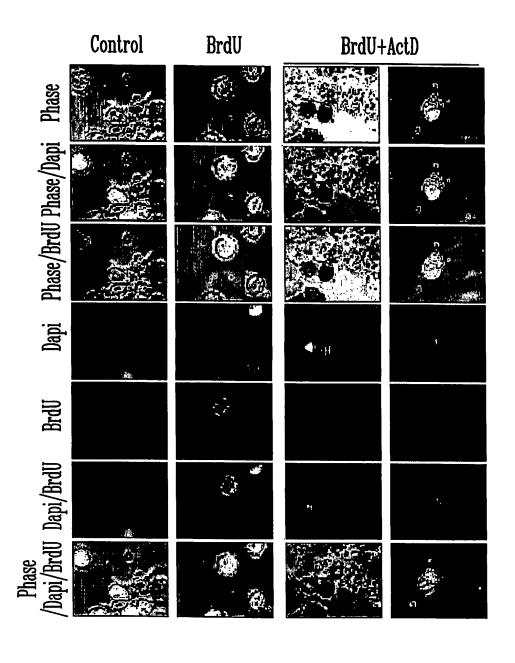


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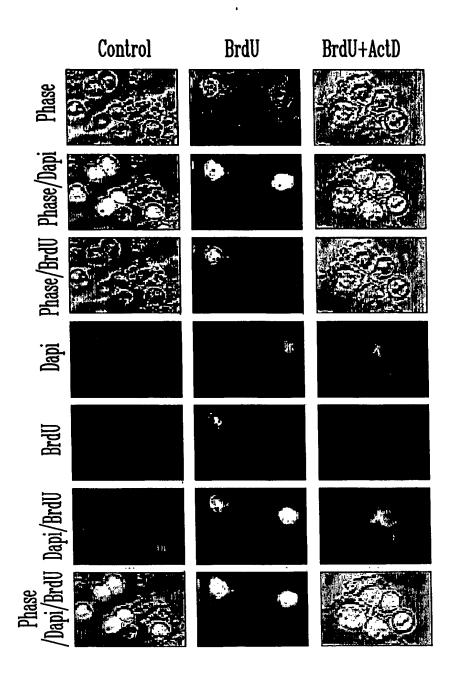
SUBSTITUTE SHEET (RULE 26)

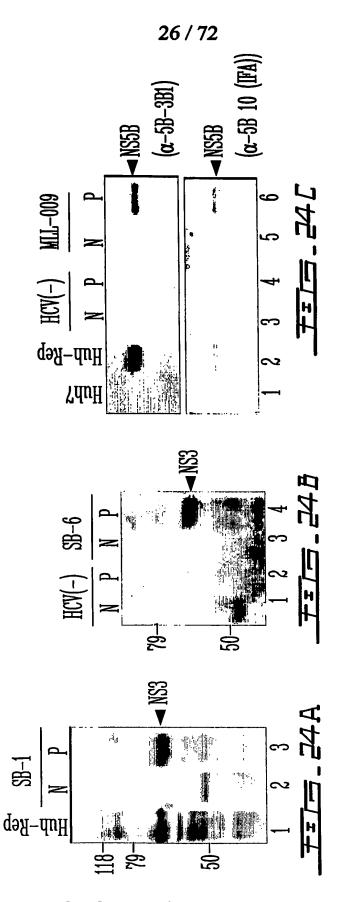
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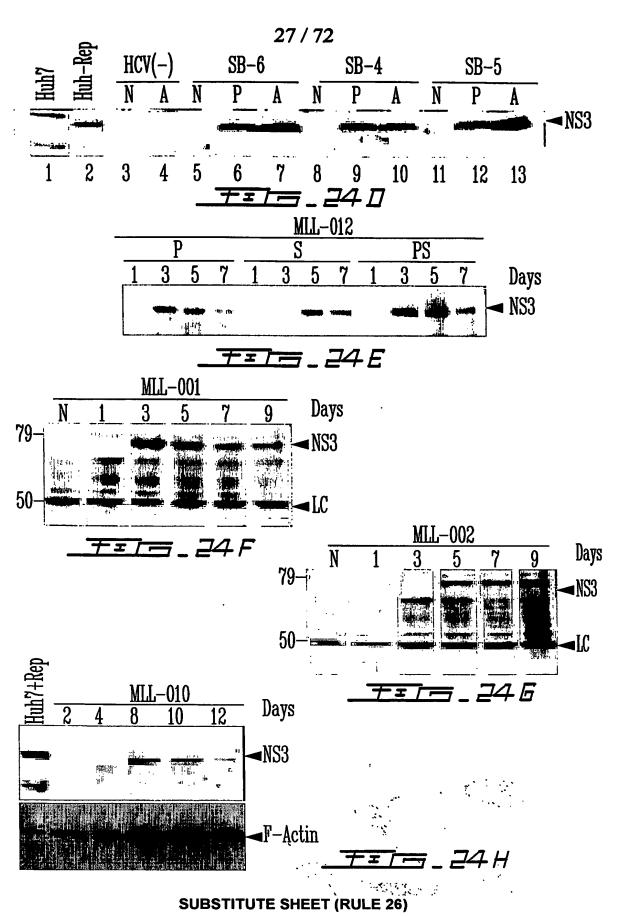
TEL- 236

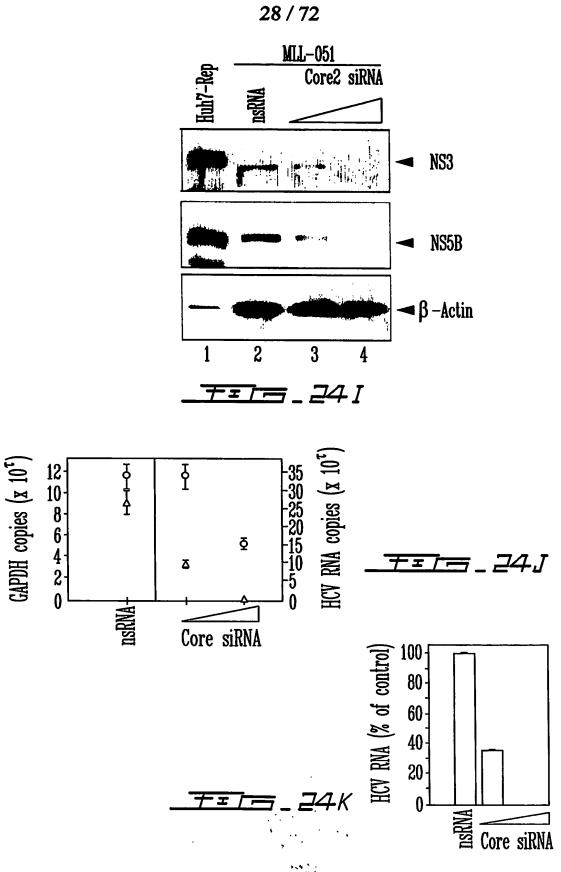
25 / 72



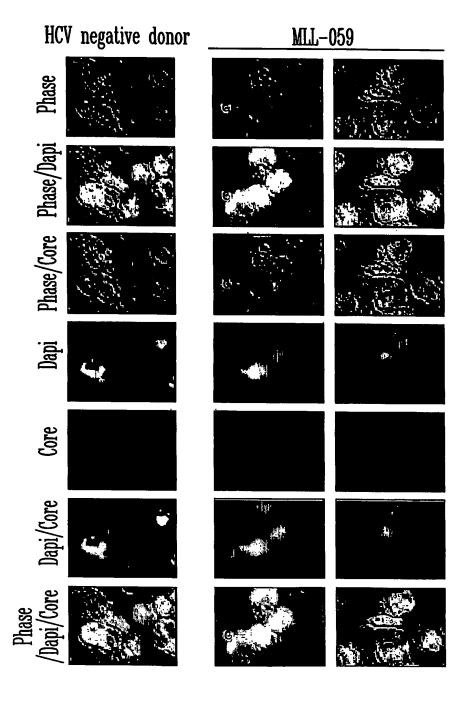


SUBSTITUTE SHEET (RULE 26)

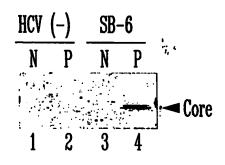


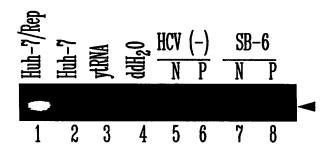


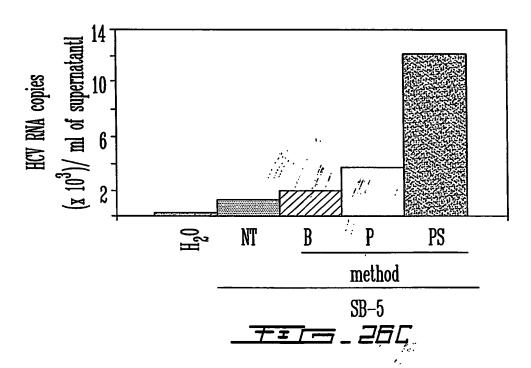
SUBSTITUTE SHEET (RULE 26)



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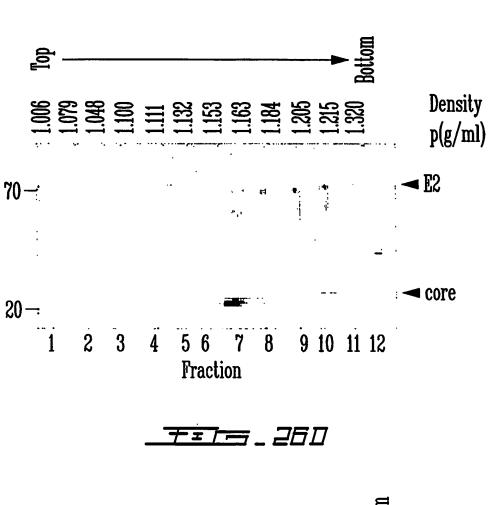


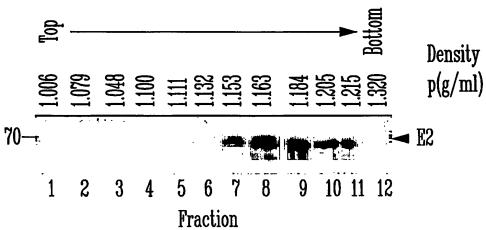


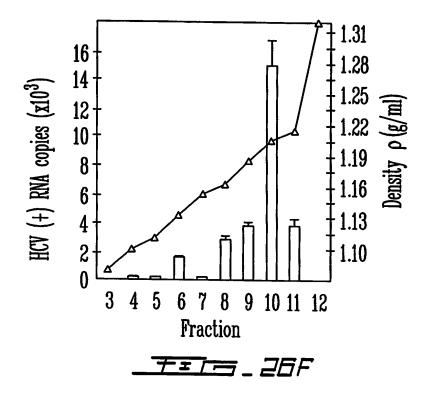


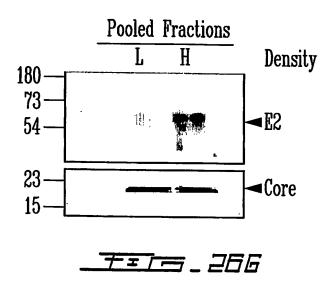
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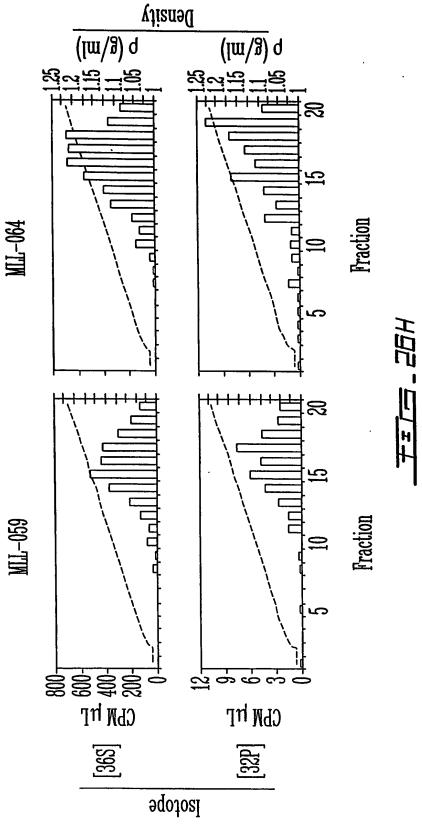






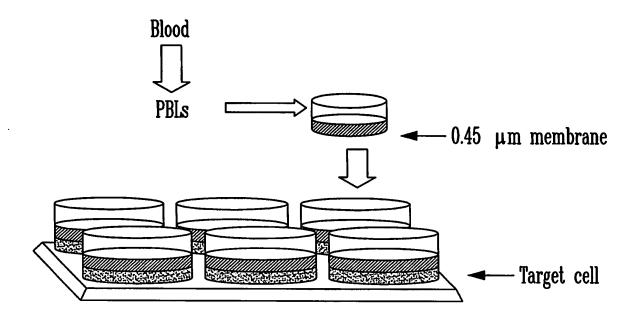


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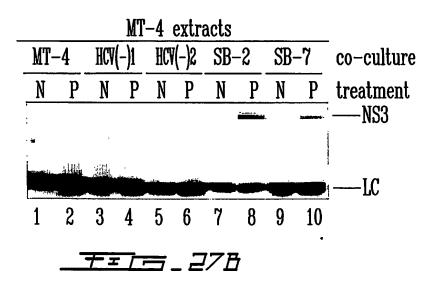


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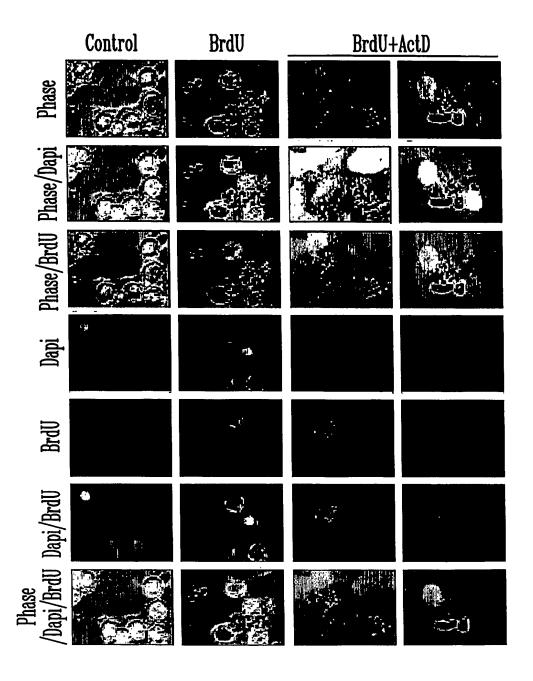
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#= 17 A

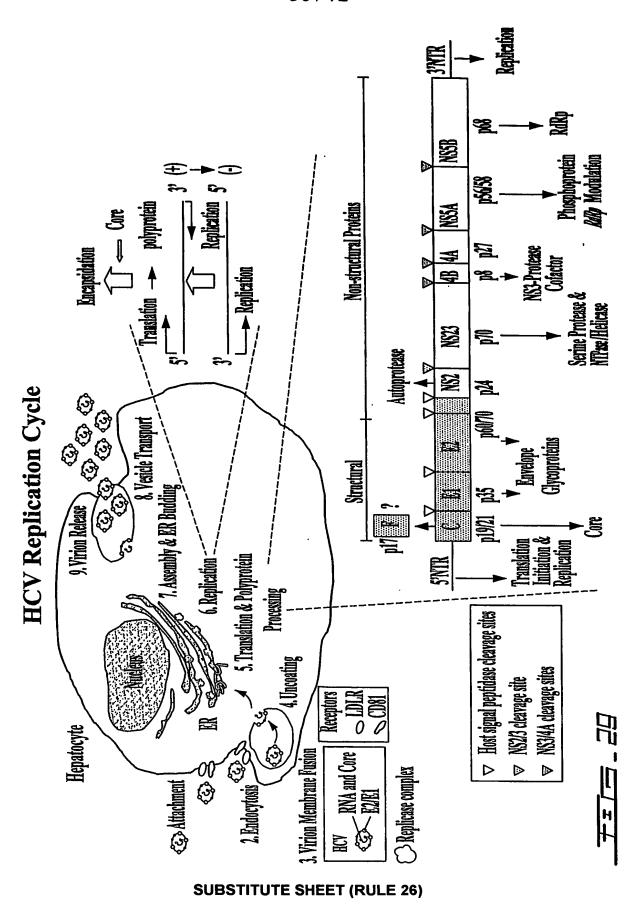


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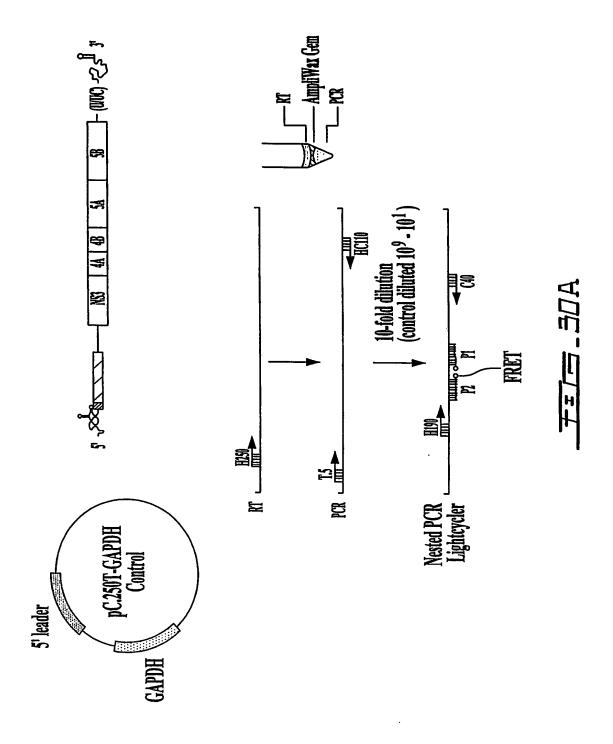


11-11-11

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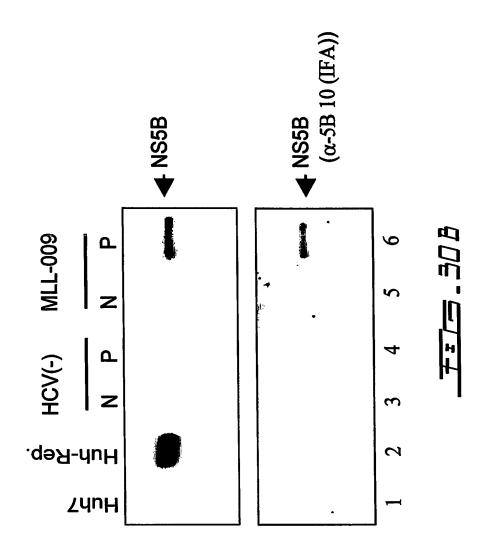


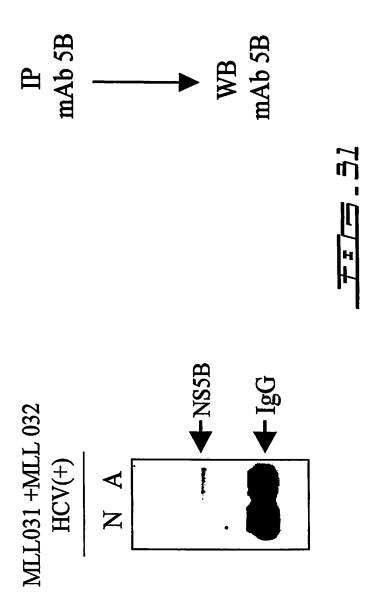
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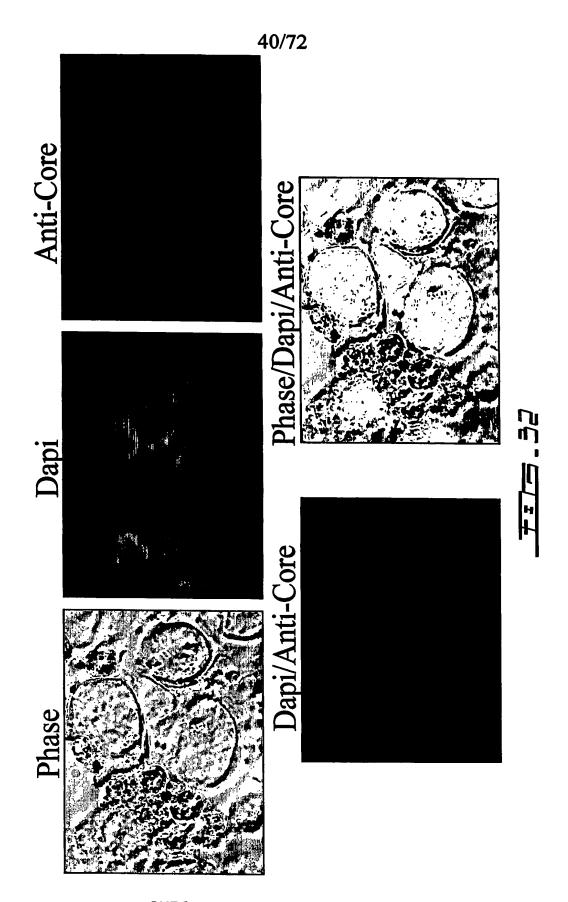
SUBSTITUTE SHEET (RULE 26)

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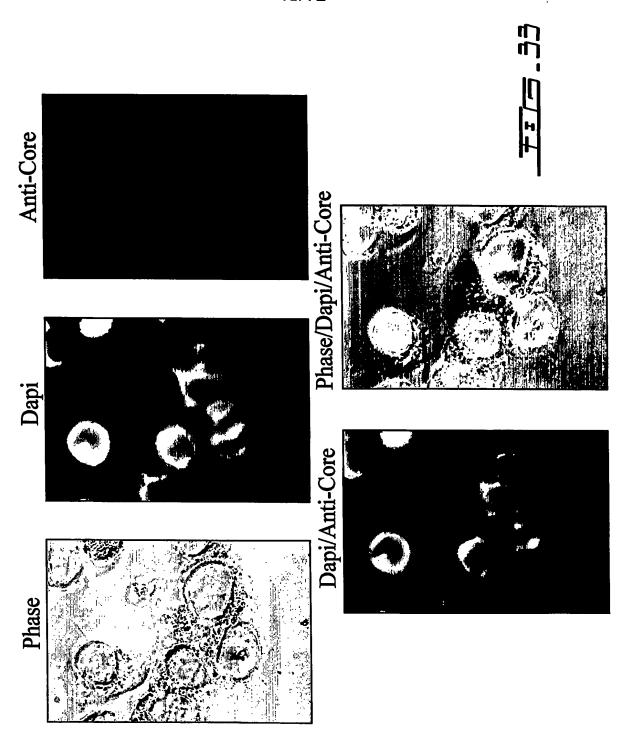


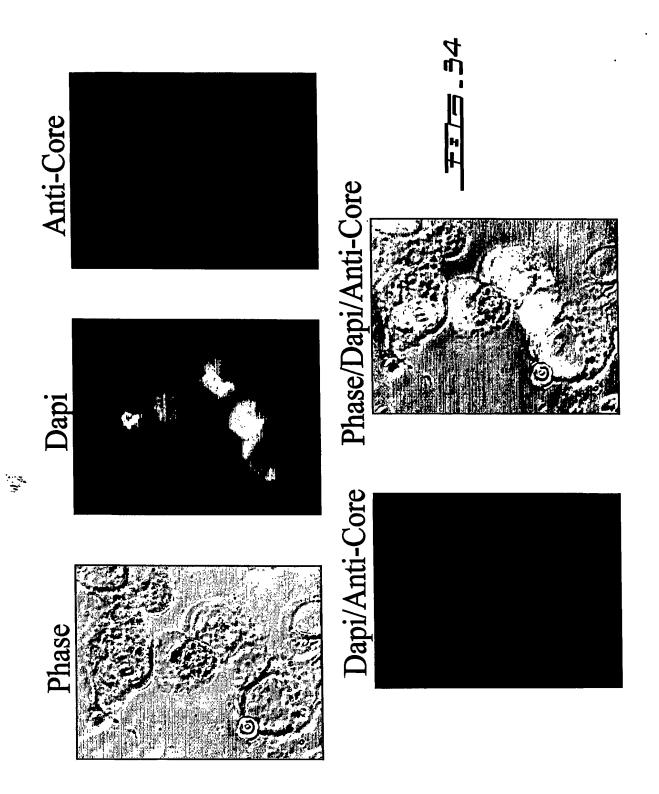


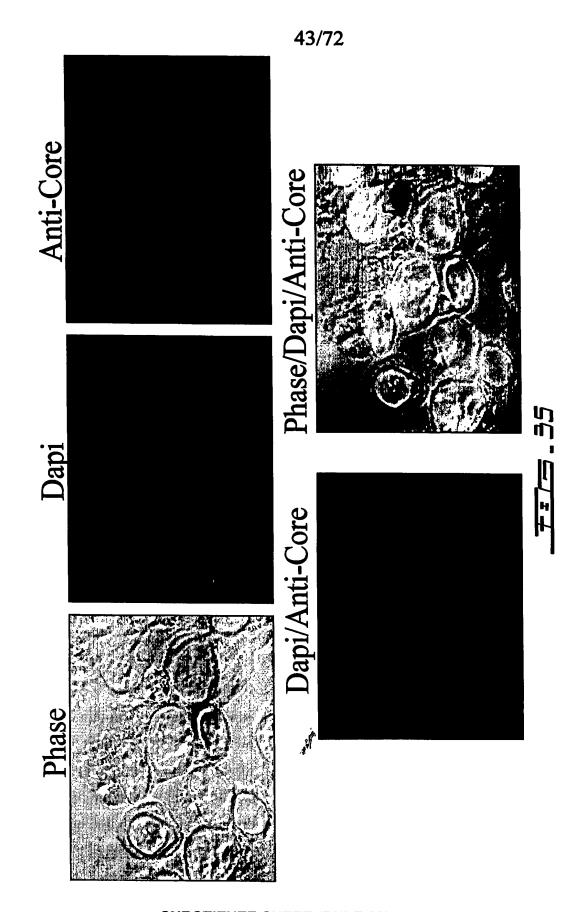
WO 2005/005625



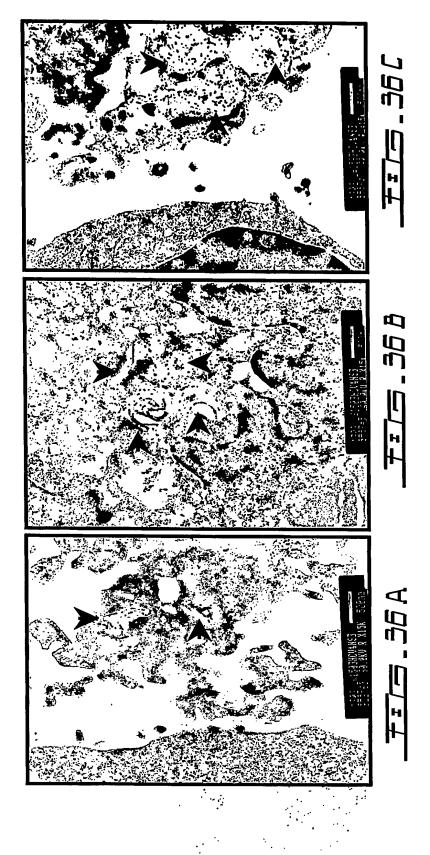
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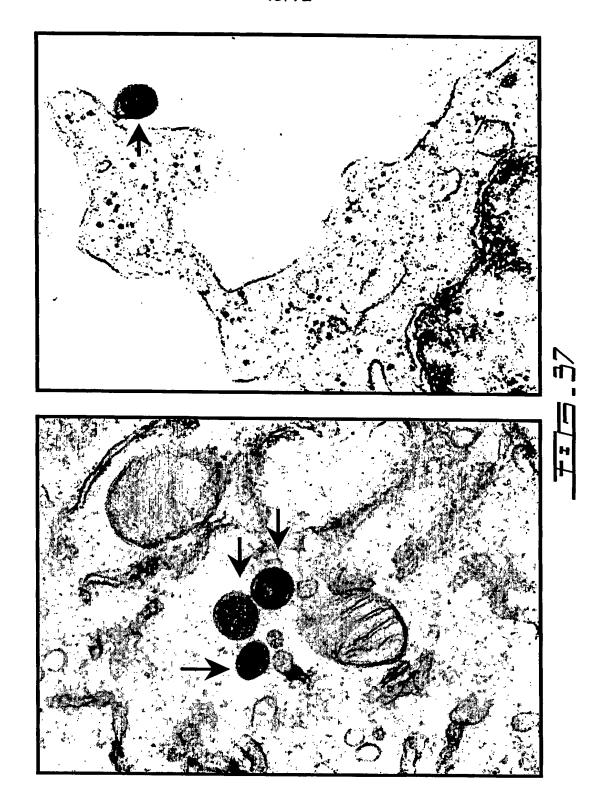




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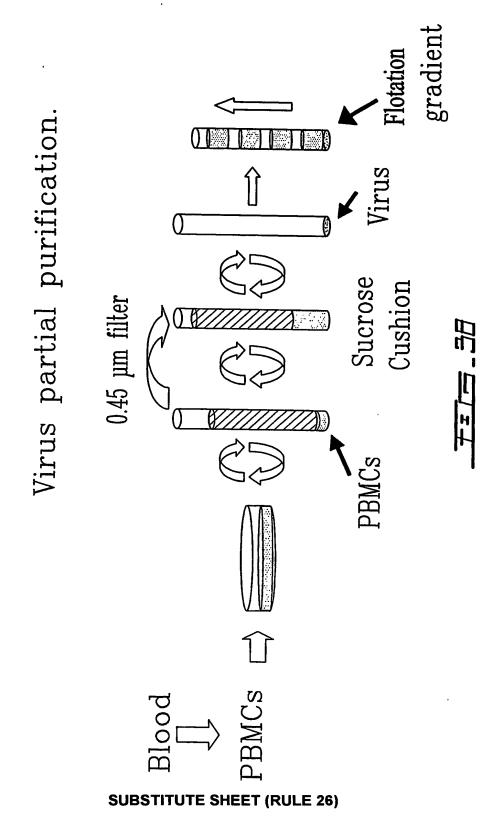


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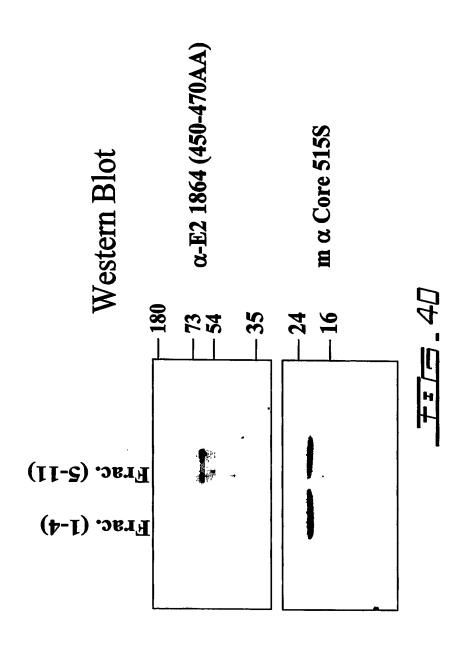


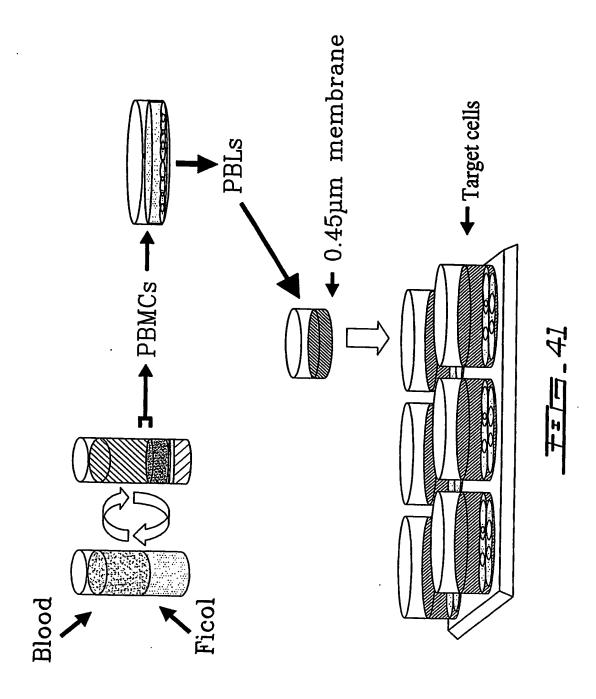
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Density Range (g/ml)	Source	Reference
1.15-1.20	HCV-LP in VSV vector	J.Virol (2002) 76, 12325.
1.14-1.18	HCV-LP in insect cells	J. Virol (1998) 72, 3827.
1.12-1.17	Plasma chimps	J. Gen. Virol (1994) 75, 1755
1.09-1.21	Plasma chimps	J.Med.Virol (1991), 34, 206.
1.13-1.17	Plasma chimps	J.Virol (1993) 67, 1953
1.063-1.21	Serum infected donors	J Med Virol (2002) 68, 335

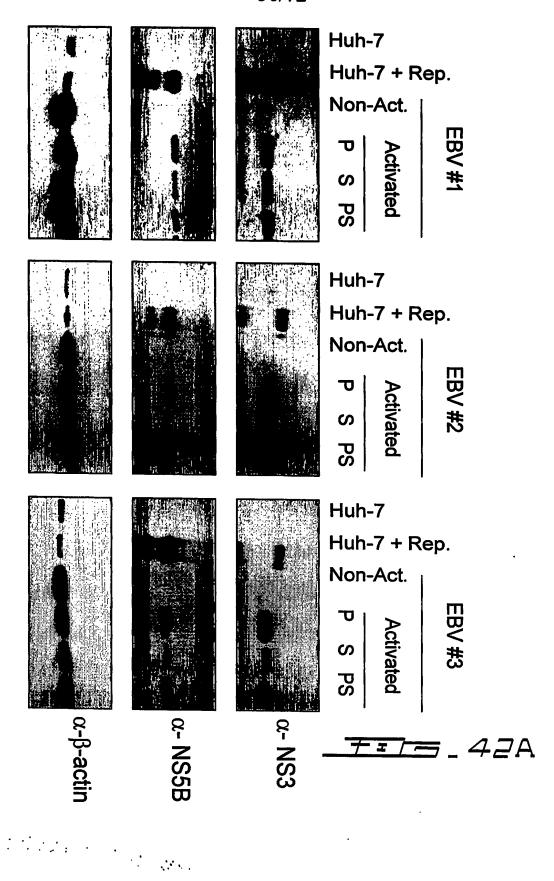
7 = (3)

HCV(+) PBMCs

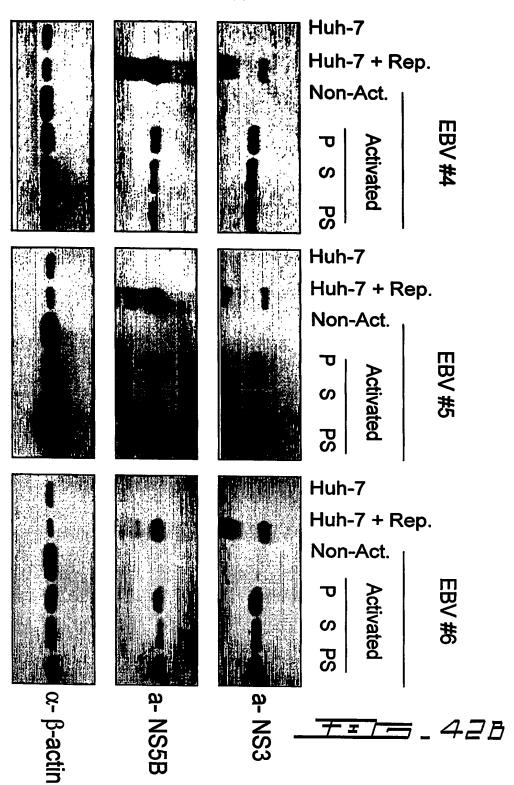


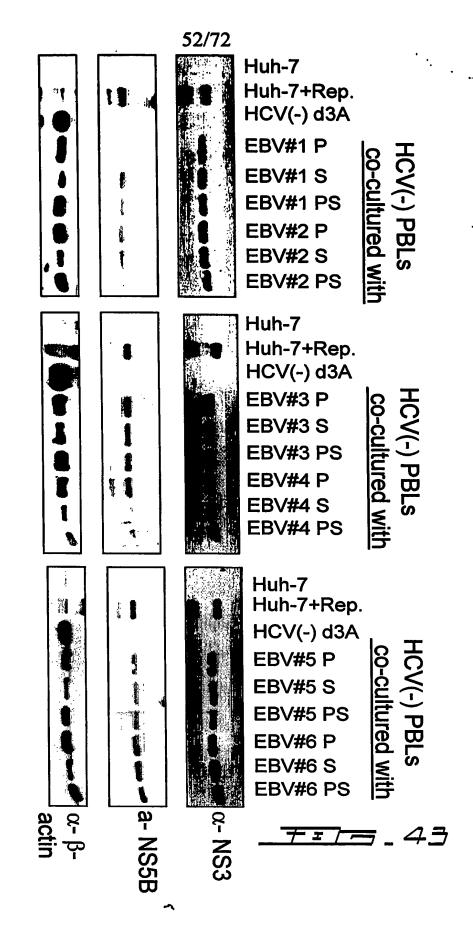


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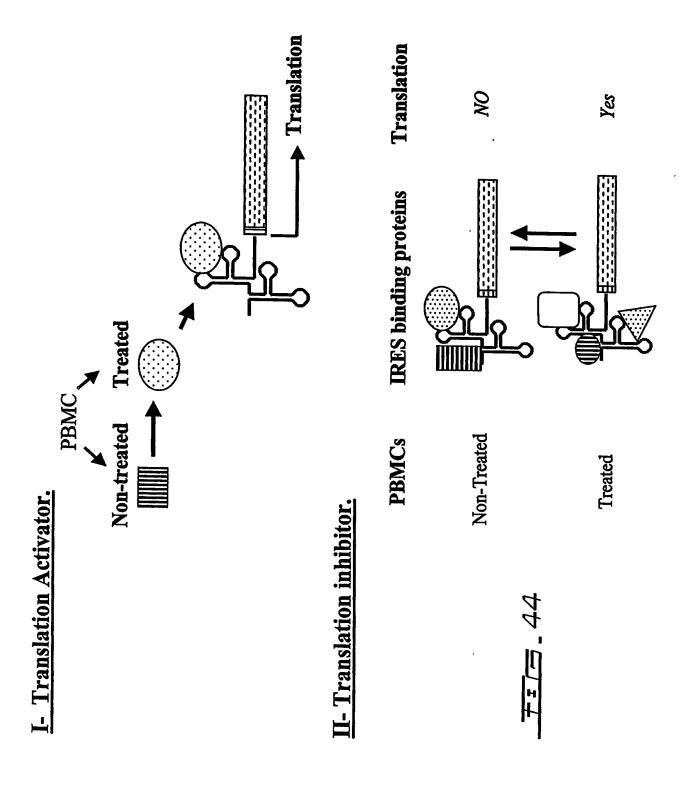


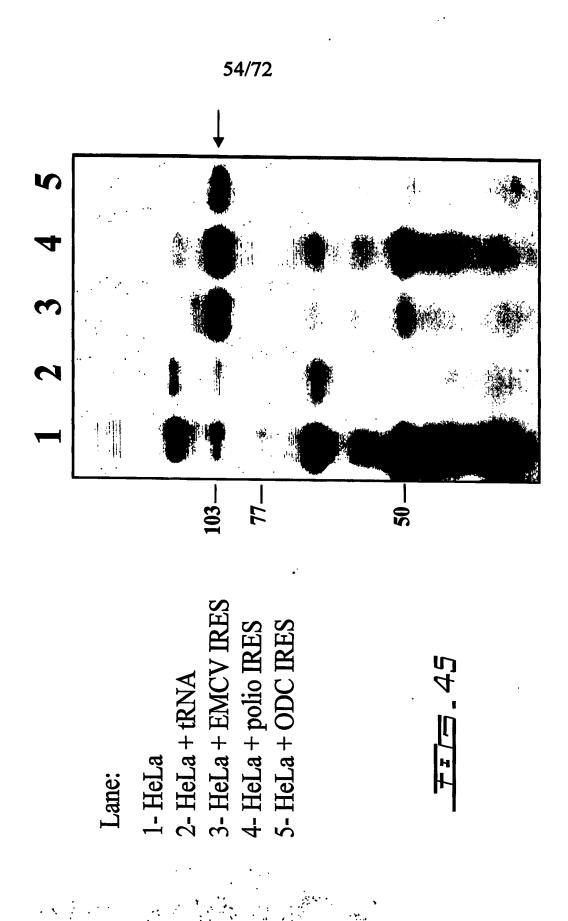
51/72

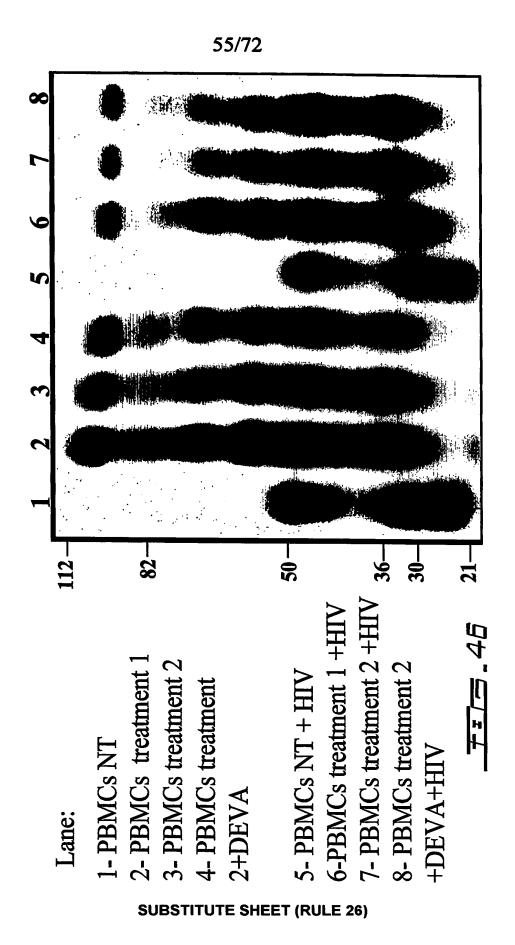


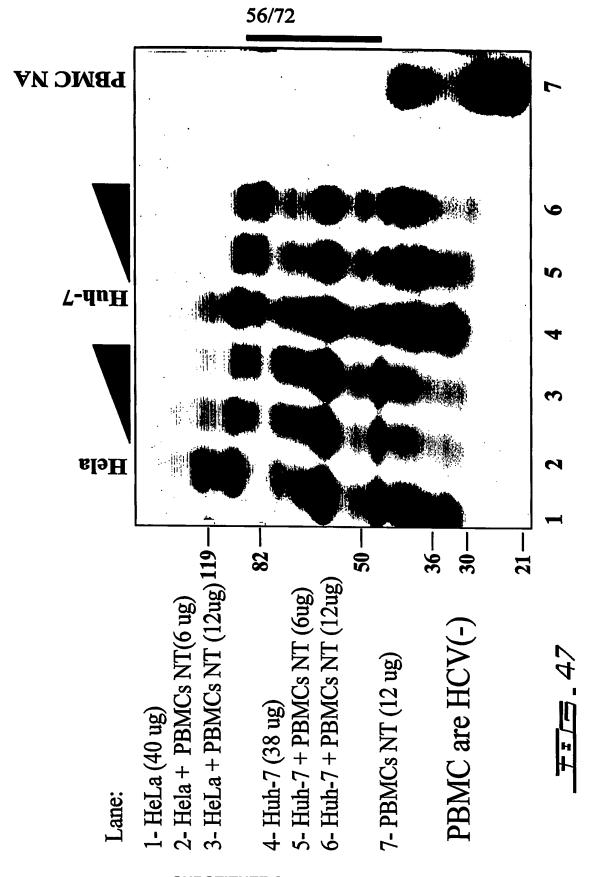


SUBSTITUTE SHEET (RULE 26)



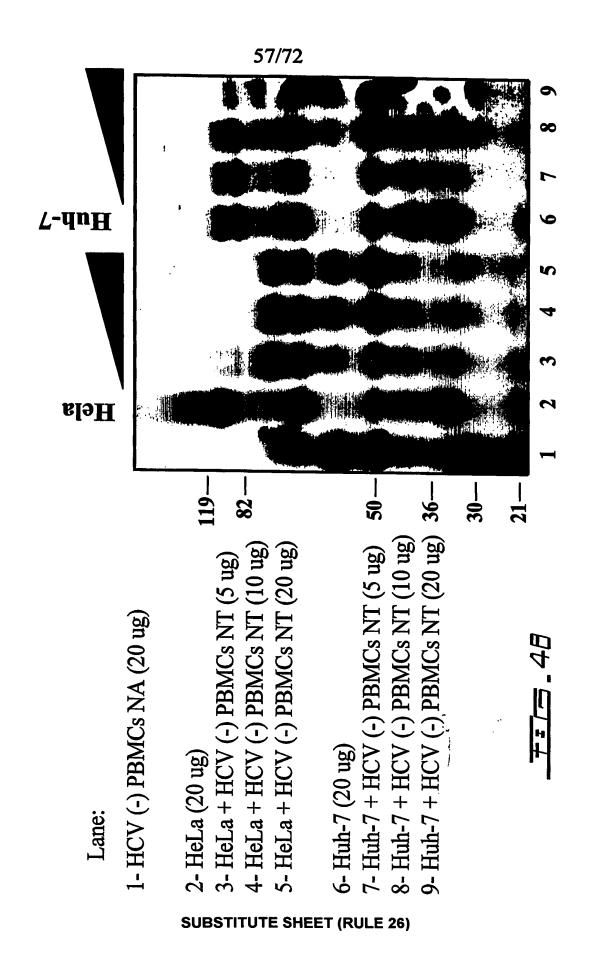


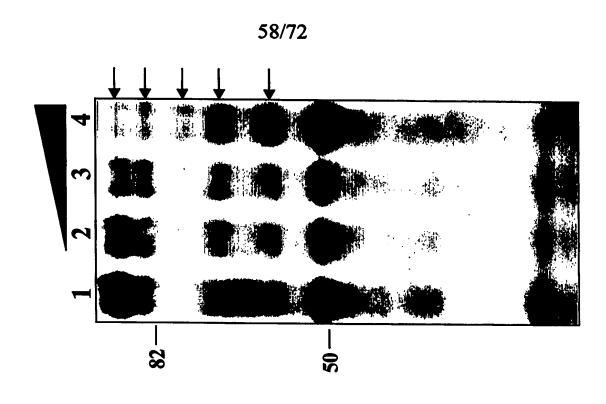




SUBSTITUTE SHEET (RULE 26)

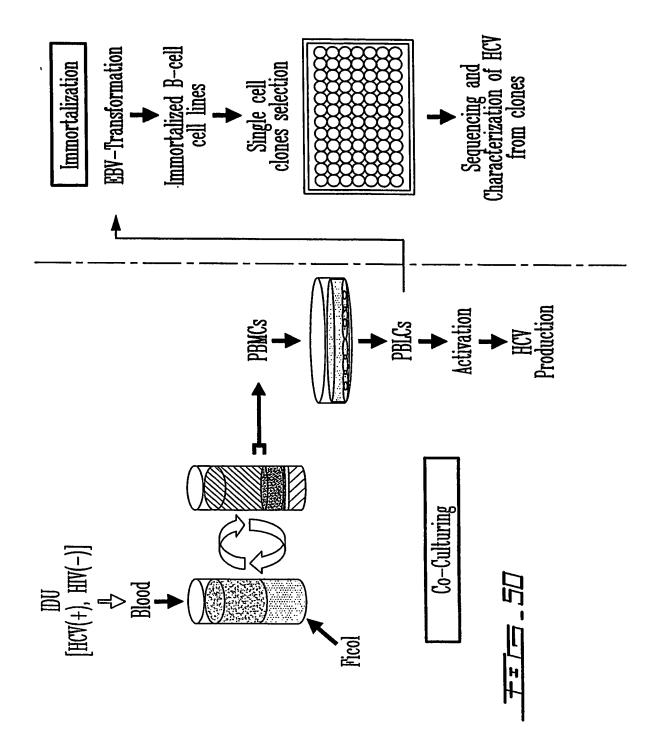
WQ 2005/005625





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1- Huh-7 (20ug)
2- Huh-7 + HCV (-) PBMCs NT (5ug)
3- Huh-7 + HCV (-) PBMCs NT (10ug)
4- Huh-7 + HCV (-) PBMCs NT (20ug)



HCV(+)- EBV-Transformed B-Cells.

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HCV (+)-EBV cell lines (Mixed population) Blood from an HCV(+) donor

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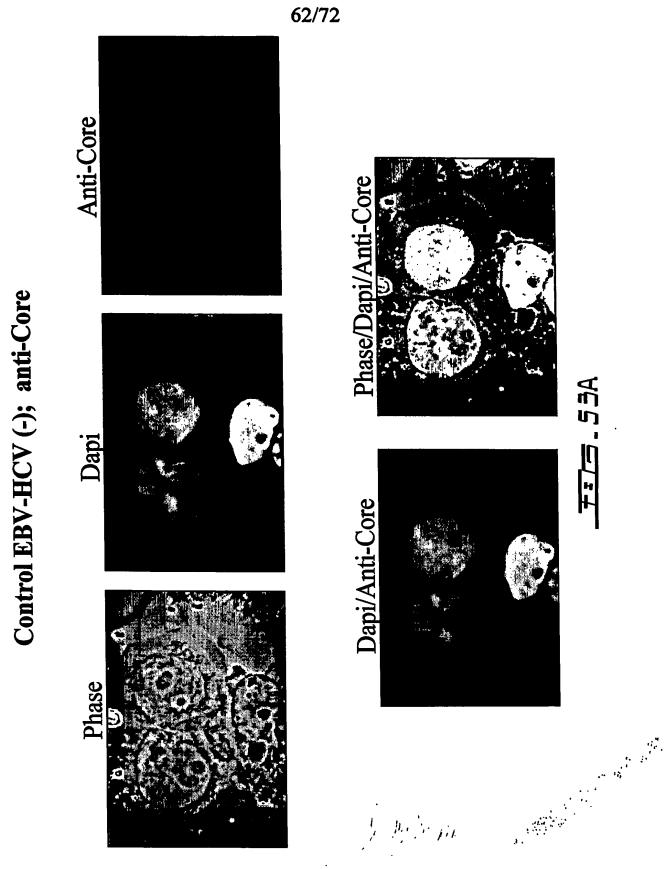
HCV RNA is detected in mixed population of EBV-transformed B-cells

HCV (+) Strand RNA

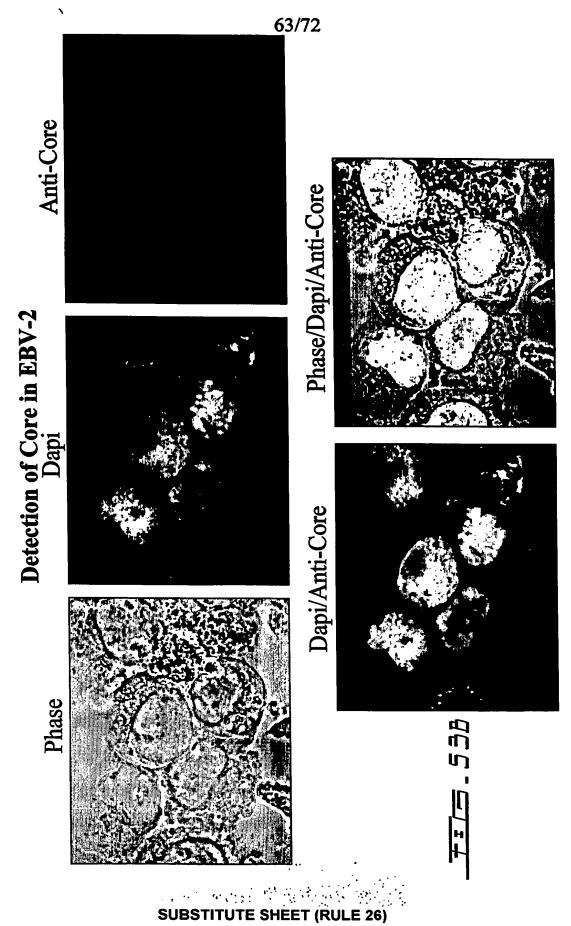
	Non-Stimulated cells	Stimulated cells
Cell line	RNA Copies /10 ⁶ cells	RNA Copies /10 ⁶ cells
EBV-1	4.66x10 ⁵	2.33x10 ⁶
EBV-2	2.77x10 ⁵	7.91x10 ⁴
EBV-3	3.96x10 ⁶	$4.02x10^{5}$
EBV-4	2.03x10 ⁶	1.57x10 ⁶
EBV-6	1.41x10 ⁶	$4.32x10^{5}$
EBV-HCV (-)	0	0

JAPDH mRNA

Cell line RNA Copies EBV-1 2.23x EBV-2 8.73x EBV-3 1.83x FRV-4 5.48x		
	RNA Copies /10 ⁶ cells	RNA Copies /10 ⁶ cells
	2.23x10 ⁸	$2.19x10^{8}$
	8.73x10 ⁸	2.25×10^{8}
	1.83x10 ⁹	$1.77 \text{x} 10^9$
	5.48x10 ⁸	3.79×10^8
EBV-6 1.26x1	1.26x10 ⁹	9.42×10^{8}
EBV-HCV (-) 9.27x1	9.27x10 ⁷	$3.62 \text{x} 10^8$



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HCV(+)-EBV cell lines Clonal

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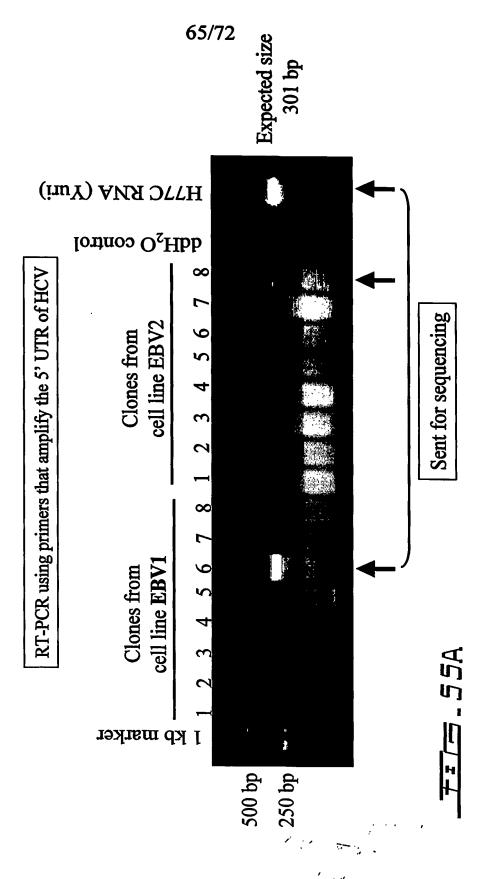
HCV (+)-EBV cell lines Mixed population

HCV(+)- EBV-Transformed B-Cells.

HCV(+) donor Blood from an

PBMCs

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SUBSTITUTE SHEET (RULE 26)

Alignment: H77C (RT-PCR positive control) sequence (top)/

EBV1 clone 6 sequence (bottom)

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ΟO

CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAGCCATGGCGT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAGCCATGGCGT

TAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCTCCCGGGAGAGCCCATAGTGGTC TAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCCCCGGGGAGAGCCATAGTGGTC

اك

TGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGAT<u>A</u>A TGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTC<u>T</u>TGGAT<u>T</u>A ACCCGCTCA CATGCCTGGAGATTTGGGCGTGCCCCCCCCAAGACTGCTAGCCGAGTAG $\mathsf{ACCCGCTCA}$ – $\mathsf{ATGCCTGGAGATTTGGGCGTGCCCCCCCGC}$ $oldsymbol{G}\mathsf{AGACTGCTAGCCGAGTAG}$

TGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGT TGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGT <u> 7=73</u>.55B

Blue: sequence from virus in the serum (MLL-005).

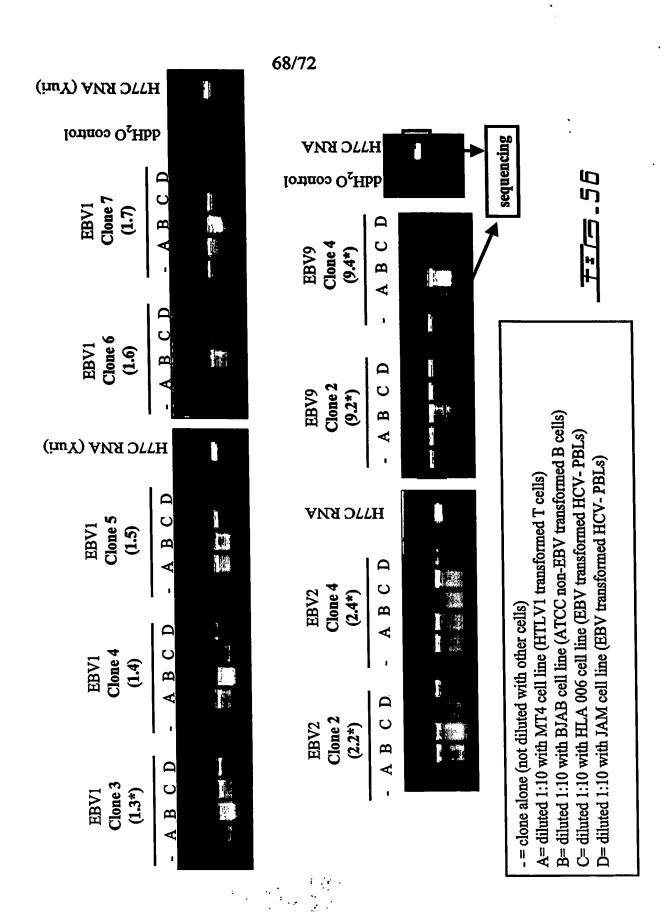
Alignment: H77C (RT-PCR positive control) sequence (top)/ CCAGGACCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACC EBV2 clone 8 sequence (bottom).

CCAGGACCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACC GGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGG GGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGG ATAAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCCGCAAG ATAAA11CCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCCGCAAG

ACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTAC ACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTAC TGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGAC $\mathtt{TGCCTGATAGGGTGCTTGCGAGTGC}_{oldsymbol{Z}\mathsf{CCGGGGAGGTCTCGTAGAC}}$

CGTGCA

T=13-55C



SUBSTITUTE SHEET (RULE 26)

Alignment of all 9.2 sequences

CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT CACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCT 9.2d final seq 9.2a final seq 9.2b final seq 9.2c final seq 9.2 final seq

9.2a final seq AGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCC 9.2b final seq AGCCATGGCGTTAGTATGAGTGTCGT $oldsymbol{\mathcal{A}}$ CAGCCTCCAGG $oldsymbol{\mathcal{C}}$ CCCCC 9.2c final seq AGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCC 9.2d final seq AGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCC 9.2 final seq AGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCC AGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCC H77C

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9.2b final seq CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC 9.2 final seq CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC 9.2a final seq CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC 9.2c final seq CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC 9.2d final seq CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC CCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACAC H77C

7515.57A

a= clone alone (not diluted with other cells)
a= diluted 1:10 with MT4 cell line (HTLV1 transformed T cells)
b= diluted 1:10 with BJAB cell line (ATCC non-EBV transformed B cells)
c= diluted 1:10 with HLA 006 cell line (EBV transformed HCV- PBLs)
d= diluted 1:10 with JAM cell line (EBV transformed HCV- PBLs)

Red= Variation with respect to clone 9.2

Alignment of all 9.2 sequences

9.2d final seq CGGAATTGCCAGGACGACCGGGTCCTTTCTTGGAT<u>T</u>AATCCGCT CGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATAAACCCGCT CGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATAAACCCGCT 9.2a final seq CGGAATTGCCAGGACGACCGGGTCCTTTCTTGGAT<u>T</u>AACCCGCT 9.2b final seq CGGAATTGCC \overline{G} GGA \overline{A} GAC \overline{T} GGGTCCTTTCTTGGATAAACCC \overline{A} CT 9.2c final seq CGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATAAACCCGCT 9.2 final seq

9.2d final seq CAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGACTGCTAGCCG CAATGCCTGGAGATTTGGGCGTGCCCCCCCCAAGACTGCTAGCCG 9.2a final seq CAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGACTGCTAGCCG 9.2c final seq CAATGCCTGGAGATTTGGGCGTGCCCCCCCCAAGACTGCTAGCCG CAATGCCTGGAGATTTGGGCGTGCCCCCCGCAAGACTGCTAGCCG 9.2b final seq CIATGCCCGGCCATTTGGGCGTGCCCCCGC \overline{A} AGACTGCTAGCCG 9.2 final sed H77C

FICE 57B

Alignment of all 9.2 sequences

AGTAGTGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG 9.2 final seq AGTAGTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG 9.2a final seq AGTAGTGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG 9.2b final seq AGTAGCGTTGGGTTGCGAAAGGCCTTGTGGTACTGCCTGATAGG 9.2c final seq AGTAGTGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG 9.2d final seq AGTAGTGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG

GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA 9.2a final seq GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA 9.2b final seq GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA 9.2c final seq GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA 9.2d final seq GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCA 9.2 final seq

